

SEQUENCE LISTING

<110> Ecole Polytechnique Fédérale de Lausanne (EPFL)

<120> Method for identification of suitable fragmentation sites in a reporter protein

<130> PEPF001WO

<150> US 34,404 JM-213

<151> 2003-10-09

<160> 66

<170> PatentIn version 3.1

<210> 1

<211> 672

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> modified_base

<222> (186)..(186)

<223> silent point mutation introduced to generate HindIII restriction site

<300>

<308> NCBI / NC_001136

<309> 2004-08-30

<400> 1

atgtctgtta ttaatttcac aggtagttct ggtccattgg tgaaagttg cggcttgcag	60
agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt	120
gtgcccaata gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttcta	180
aaagcatata aaaatagttc aggactccg aaatacttgg ttggcgtgtt tcgtaatcaa	240
cctaaggagg atgttttggc tctggtaat gattacggca ttgatatcgt ccaactgcac	300
ggagatgagt cgtggcaaga ataccaagag ttccctcggtt tgccagttat taaaagactc	360
gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcggtt	420
atccccttgtt ttgattcaga agcaggtggg acaggtgaac ttttggattg gaactcgatt	480
tctgactggg ttgaaaggca agagagcccc gagagcttac attttatgtt agctggtgga	540
ctgacgccag aaaatgttgg tcatgcgtt agattaaatg gcgttattgg tggatgtta	600
agcggaggtg tggagacaaa tgggtaaaaa gactctaaca aaatagcaaa ttctgtcaaa	660
aatgctaaga aa	672

<210> 2

<211> 224

<212> PRT

<213> *Saccharomyces cerevisiae*

<300>

<308> NCBI / NC_001136

<309> 2004-08-30

<400> 2

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val			
1	5	10	15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp		
20	25	30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile		
35	40	45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys		
50	55	60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu
180 185 190

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly
195 200 205

Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
210 215 220

<210> 3

<211> 132

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> modified_base

<222> (22)..(22)

<223> point mutation

<400> 3

atgtctgtta ttaatttcac atgttagttct ggtccattgg tgaaagttg cggcttgcag 60
agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120
gtgcccaata ga 132

<210> 4

<211> 44

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 4

Met Ser Val Ile Asn Phe Thr Cys Ser Ser Gly Pro Leu Val Lys Val
1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg
35 40

<210> 5

<211> 540

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 5
aagagaacaa ttgaccgggt tattgcaagg aaaatttcaa gtcttgtaaa agcatataaa 60
aatagttcag gcactccgaa atactgggtt ggctgtttc gtaatcaacc taaggaggat 120
gttttggctc tggtaatga ttacggcatt gatatcgcc aactgcacgg agatgagtgc 180
tggcaagaat accaagagtt cctcggttg ccagttatta aaagactcgt atttccaaaa 240
gactgcaaca tactactcag tgcagcttca cagaaacctc attcgtttat tcccttggtt 300
gattcagaag caggtggac aggtgaactt ttggattgga actcgatttc tgactgggtt 360
ggaaggcaag agagccccga gagcttacat tttatgttag ctgggtggact gacgccagaa 420
aatgttggtg atgcgcttag attaaatggc gttattgggt tgatgttaag cggaggtgtg 480
gagacaaatg gtgtaaaaga ctctaacaaa atagcaaatt tcgtaaaaa tgctaagaaa 540

<210> 6

<211> 180

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 6

Lys Arg Thr Ile Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val
1 5 10 15

Lys Ala Tyr Lys Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val
20 25 30

Phe Arg Asn Gln Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr
35 40 45

Gly Ile Asp Ile Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr
50 55 60

Gln Glu Phe Leu Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys
65 70 75 80

Asp Cys Asn Ile Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe
85 90 95

Ile Pro Leu Phe Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp
100 105 110

Trp Asn Ser Ile Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser
115 120 125

Leu His Phe Met Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp
130 135 140

Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val
145 150 155 160

Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys
165 170 175

Asn Ala Lys Lys
180

<210> 7

<211> 159

<212> DNA

<213> Saccharomyces cerevisiae

<400> 7

atgtctgtta ttaatttcac aggtagttct ggtccattgg tgaaagtttgcggcttgcag 60

agcacagagg ccgcagaatg tgctcttagat tccgatgctg acttgctggg tattatatgt 120

gtgcccaata gaaagagaac aattgacccg gttattgca 159

<210> 8

<211> 53

<212> PRT

<213> Saccharomyces cerevisiae

<400> 8

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
35 40 45

Asp Pro Val Ile Ala
50

<210> 9

<211> 516

<212> DNA

<213> Saccharomyces cerevisiae

<400> 9

gcaaggaaaa ttcaagtct tgtaaaagct tataaaaata gttcaggcac tcggaaatac 60

ttggttggcg tgttcgtaa tcaacctaag gaggatgttt tggctctggt caatgattac 120

ggcattgata tcgtccaaact gcacggagat gagtcgtggc aagaatacca agagttcctc	180
ggtttgcag ttattaaaag actcgtattt ccaaaagact gcaacatact actcagtgc	240
gcttcacaga aacctcattc gtttattccc ttgtttgatt cagaaggcagg tggacaggt	300
gaactttgg attggaactc gatttctgac tgggttgaa ggcaagagag ccccgagagc	360
ttacattta tgttagctgg tggactgac ccagaaaatg ttggtgatgc gcttagatta	420
aatggcgtta ttggtgtga tgtaagcgg a ggtgtggaga caaatggtgt aaaagactct	480
aacaaaatag caaatttcgt caaaaatgct aagaaa	516

<210> 10

<211> 172

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 10

Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys Asn Ser Ser Gly					
1	5		10		15
	10				
	15				

Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln Pro Lys Glu Asp			
20	25		30
	30		

Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile Val Gln Leu His			
35	40		45
	45		

Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu Gly Leu Pro Val			
50	55		60
	60		

Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile Leu Leu Ser Ala					
65	70		75		80
	75		80		
	80				

Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe Asp Ser Glu Ala			
85	90		95
	95		

Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile Ser Asp Trp Val			
100	105		110
	110		

Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met Leu Ala Gly Gly			
115	120		125
	125		

Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu Asn Gly Val Ile			
130	135		140
	140		

Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly Val Lys Asp Ser
145 150 155 160

Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
165 170

<210> 11

<211> 561

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 11
atgtctgtta ttaatttcac aggtagttct ggtccattgg tgaaagtttgcggcttg 60
agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120
gtgcccaata gaaagagaac aattgaccgg gttattgcaa ggaaaatttc aagtcttgta 180
aaagcttata aaaatagttc aggcaactccg aaatacttgg ttggcggtt tcgtaatcaa 240
cctaaggagg atgttttggc tctggtaat gattacggca ttgatatcgt ccaactgcac 300
ggagatgagt cgtggcaaga ataccaagag ttctcggtt tgccagttat taaaagactc 360
gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcg 420
attcccttgtt ttgattcaga agcaggtggg acaggtgaac ttttggatttgaactcg 480
tctgactggg ttgaaaggca agagagcccc gagagcttac attttatgtt agctggtg 540
ctgacgcccag aaaatgttgg 561

<210> 12

<211> 187

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 12

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
35 40 45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
50 55 60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly
180 185

<210> 13

<211> 111

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 13
gatgcgctta gattaaatgg cgttatttgtt gttgatgtaa gcggaggtgt ggagacaaat 60
ggtgtaaaag actctaacaa aatagcaaat ttcgtcaaaa atgctaagaa a 111

<210> 14

<211> 37

<212> PRT

<213> Saccharomyces cerevisiae

<400> 14

Asp Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly
1 5 10 15

Val Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val
20 25 30

Lys Asn Ala Lys Lys
35

<210> 15

<211> 612

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> mutation

<222> (22)..(22)

<223> point mutation

<220>

<221> deletion

<222> (612)..(612)

<223> missing sequence after base 612 of wild-type: GAGACAAATGGTGTAAAAG
ACTCT

<400> 15

atgtctgtta ttaatttcac atgttagttct ggtccattgg tgaaagtttgcggcttgca 60

agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120

gtgcccaata gaaagagaac aattgaccgg gttattgcaa ggaaaatttc aagtcttcta 180

aaagcttata aaaatagttc aggcactccg aaatacttgg ttggcgtgtt tcgtaatcaa 240

cctaaggagg atgtttggc tctggtaat gattacggca ttgatatacg ccaactgcac	300
ggagatgagt cgtggcaaga ataccaagag ttcctcggtt tgccagttat taaaagactc	360
gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcggtt	420
attcccttgtt ttgattcaga agcaggtggg acaggtgaac ttttgattg gaactcgatt	480
tctgactggg ttggaaggca agagagcccc gagagcttac attttatgtt agctggtgga	540
ctgacgccag aaaatgttgg tcatgcgcctt agattaaatg gcgttattgg tggatgtta	600
agcggagggtg tg	612

<210> 16

<211> 204

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 16

Met Ser Val Ile Asn Phe Thr Cys Ser Ser Gly Pro Leu Val Lys Val					
1	5		10		15
	10				
	15				

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp			
20	25		30
	30		

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile			
35	40		45
	45		

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys			
50	55		60
	60		

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln					
65	70		75		80
	75		80		
	80				

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile			
85	90		95
	95		

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu			
100	105		110
	110		

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile			
115	120		125
	125		

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe			
130	135		140
	140		

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu
180 185 190

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val
195 200

<210> 17

<211> 36

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> mutation

<222> (1)..(1)

<223> missing sequence before base 1 of SEQ17, corresponding to base 63
7 of wild-type: GAGACAAATGGTGTAAAAGACTCT

<400> 17

aacaaaatag caaatttcgt caaaaatgct aagaaa 36

<210> 18

<211> 12

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 18

Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
1 5 10

<210> 19

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> first of a pair of peptides (together with peptide C2), that associate into an anti-parallel coiled coil (Biochemistry 37 (1998), 12603-12610)

<400> 19

Met Asp Tyr Lys Asp Glu Ser Gly Gln Ala Leu Glu Lys Glu Leu Ala
1 5 10 15

Gln Asn Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Leu
20 25 30

Glu Lys Glu Leu Gln Ala Gly Ser Gly Ser Gly
35 40

<210> 20

<211> 50

<212> PRT

<213> Artificial Sequence

<220>

<223> second of a pair of peptides (together with peptide C1), that associate into an anti-parallel coiled coil (Biochemistry 37 (1998), 12603-12610)

<400> 20

Gly Gly Ser Gly Ser Gly Gln Ala Leu Lys Lys Lys Leu Ala Gln Leu
1 5 10 15

Lys Trp Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Lys
20 25 30

Lys Leu Gln Ala Gly Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ala
35 40 45

Phe Leu
50

<210> 21
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for Ctrp fusions

<400> 21
cgatacgaat tcatggacaa ggatttgtaa atgaaacgc 39

<210> 22
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for pRS316-C1/2CUP1

<400> 22
aaaggaattg gcccaaaatg agtgggagtt acaagcactt gagaa 45

<210> 23
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for pRS316-C1/2CUP1

<400> 23
ctcaatgttc gtgaactctt cctcgagcga gttgaactct tcctc 45

<210> 24
<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 24

ctccttctca agttgagcga gtccttctc aagtgcgtgt aactc

45

<210> 25

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 25

ggcacttaag aagaagttgg cgtagctaa gtggaaactg ca

42

<210> 26

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 26

agctggccat tcttcttctt aagagcttgc agttccact taagct

46

<210> 27

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 27

aagaagaaga atgcccagct taagaagaag ctccaggctg gaagttac

48

<210> 28

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 28

atacgatgtt ccagattacg ctgcattttt ataagtgcac tggtc

45

<210> 29

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 29

gaccagtgcga cttataaaaaa tg

22

<210> 30

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for circular permutation of TRP1

<400> 30

gtaaaaagctt ataaaaatag ttcag

25

<210> 31
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for circular permutation of TRP1
<400> 31
gaaatagcct aggatgtctg ttattaattt cacagg 36

<210> 32
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for circular permutation of TRP1
<400> 32
cagacatcct aggctatttc ttagcatttt tgacg 35

<210> 33
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for circular permutation of TRP1
<400> 33
tttataagct tttacaagac ttgaa 25

<210> 34
<211> 22
<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 34

gtaacgaatt catggactac aa

22

<210> 35

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 35

cattttgggc caattcctt tccagtgtt gaccactttc gtcttttag tcctatgaatt

60

cgttac

66

<210> 36

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 36

caaccttcttc ttaagtgcct gacctgatcc agatccacccg ttaaacacctg aacctgatcc

60

ggcc

64

<210> 37

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 37

gtaatctgga acatcgatg ggtaacttcc agcctggagc ttc

43

<210> 38

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for homologous recombination

<400> 38

gactctaaca aaatagcaaa ttgcgtcaaa aatgctaaga aatagagggc cgcatcatgt

60

aattag

66

<210> 39

<211> 65

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for homologous recombination

<400> 39

aactttcacc aatggaccag aactacctgt gaaattaata acagacattt tgagatccgg

60

gtttt

65

<210> 40

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 40

gcctgatcca gatccgcctt ctgggtgattc atcatcttca

40

<210> 41

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 41

ggcggatctg gatcaggcaa gagaacaatt gacccggta

40

<210> 42

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 42

gcctgatcca gatccgccta taaaaggat tccgacacca

40

<210> 43

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ntrp fusions

<400> 43

gcctgatcca gatccgcctg caataaccgg gtcaattgt

39

<210> 44
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for Ctrp fusions

<400> 44
ggcggatctg gatcaggcgcaaggaaaatt tcaagtcttgc 40

<210> 45
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for Ntrp fusions

<400> 45
gcctgatcca gatccgccac caacatttc tggcgtcagt cc 42

<210> 46
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for Ctrp fusions

<400> 46
ggcggatctg gatcaggcgatgcgtttaga tttaatggc 39

<210> 47
<211> 39
<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ntrp fusions

<400> 47

gcctgatcca gatccggcca cacctccgct tacatcaac

39

<210> 48

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 48

ggcggatctg gatcaggcaa caaaatag

28

<210> 49

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS315CUP1/ pRS316CUP1

<400> 49

agcaggatcc cattaccgac atttg

25

<210> 50

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS315CUP1/ pRS316CUP1

<400> 50

ccttaggttga gatcttttga attcgttaca gtttgaaaaa c

41

<210> 51

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS315CUP1/ pRS316CUP1

<400> 51

aattcaagag atctcaacct aggatgacgg tgggaggctata

43

<210> 52

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS315CUP1/ pRS316CUP1

<400> 52

cgattgtcga cggttgtacg ctaacgcttc tcgttgggt ctgg

45

<210> 53

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 53

acttgtcgac tcagtttgt tcggctttt cattga

36

<210> 54
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for Ctrp fusions
<400> 54
agatagatct atgcctacaa attacgagta tga 33

<210> 55
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
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